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(FILE 'HOME' ENTERED AT 10:55:02 ON 23 JUN 2003)

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SEA BETA-GLUCOSIDASE

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FILE 'CAPLUS, BIOSIS, SCISEARCH, MEDLINE, EMBASE, PASCAL, BIOTECHDS,
 CABA, LIFESCI, BIOTECHNO, TOXCENTER' ENTERED AT 10:56:49 ON 23 JUN 2003

L2 3068 S L1 AND (TRICHODERMA OR REESEI)
 L3 993 S L2 AND (PURIF? OR CHARACT? OR CLON?)
 L4 7 S L2 AND (BGL4 OR BGL4)
 L5 1 DUP REM L4 (6 DUPLICATES REMOVED)
 L6 15 S L1 AND BGL4
 L7 3 DUP REM L6 (12 DUPLICATES REMOVED)

L7 ANSWER 1 OF 3 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 2002:597055 BIOSIS
 DOCUMENT NUMBER: PREV200200597055
 TITLE: Genomic studies of cell wall-associated synthases and hydrolases of *Coccidioides immitis*.
 AUTHOR(S): Delgado, N. (1); Yu, J. J. (1); Hung, C. Y. (1); Nila, A. G. (1); Schaller, R. (1); Okeke, C. N. (1); Chen, X. (1); Cole, G. T. (1)
 CORPORATE SOURCE: (1) Medical College of Ohio, Toledo, OH USA
 SOURCE: Abstracts of the General Meeting of the American Society for Microbiology, (2002) Vol. 102, pp. 201.
<http://www.asmtusa.org/mtgsrsrc/generalmeeting.htm>. print.
 Meeting Info.: 102nd General Meeting of the American Society for Microbiology Salt Lake City, UT, USA May 19-23, 2002 American Society for Microbiology
 . ISSN: 1060-2011.
 DOCUMENT TYPE: Conference
 LANGUAGE: English
 AB The fungal kingdom comprises a large group of uni- and multicellular eukaryotic organisms whose genomes range in size from 13-42 megabases (Mb). *Coccidioides immitis* (29 Mb genome) is characterized by a unique parasitic cycle in which inhaled arthroconidia grow isotropically and differentiate into large multinucleate spherules. The latter undergo segmentation and give rise to a multiplicity of endospores. These morphogenetic events involve major alterations in cell wall architecture. The *C. immitis* genome-sequencing project (more than 1X coverage at present) has revealed multiple families of genes which encode cell wall synthases and putative cell wall modifying enzymes (hydrolases). Representative genes include 4 glucan synthases (GLS), 6 chitin synthases (CHS), 7 **beta-glucosidases** (BGL), 3 **beta-glucanotransferases** (GEL), and 6 chitinases (CTS). We speculate that the coordinated regulation of expression of these enzymes is a requirement for appropriate development of parasitic cells. Macroarray hybridization studies have revealed upregulation of GLS3 (7.4-fold), BGL2 (3X), BGL5 (5X), BGL7 (3X), GEL1 (2.5X), and CTS1 (251X) in the endospore stage compared to the isotropic growth stage. Expression of the BGL1 gene is upregulated 3-fold in the segmentation stage compared to the isotropic growth stage. Expression of BGL4, CHS4, CHS5, and CHS6 show little variation throughout the parasitic phase. These families of *C. immitis* genes have extensively studied homologues in the *Neurospora crassa* (40 Mb) and *Aspergillus fumigatus* (30-35 Mb) genomes. On the other hand, *C. immitis* genes have been identified which show no homologues in the yeast or filamentous fungal genomes (e.g., genes which encode a spherule outer wall glycoprotein (SOWgp), and the *Coccidioides*-specific antigen (CSA)). Availability of the complete *C. immitis* genomic sequence will contribute to our understanding of the uniqueness of the parasitic cycle of this fungus, and help in the identification of potential molecular targets for development of novel antifungal drugs against coccidioidomycosis.

L7 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 1
 ACCESSION NUMBER: 1999:348867 CAPLUS
 DOCUMENT NUMBER: 131:155115
 TITLE: Molecular cloning and expression of the novel fungal **beta.-glucosidase** genes from *Humicola grisea* and *Trichoderma reesei*
 AUTHOR(S): Takashima, Shou; Nakamura, Akira; Hidaka, Makoto; Masaki, Haruhiko; Uozumi, Takeshi
 CORPORATE SOURCE: Department of Biotechnology, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Tokyo, 113-8657, Japan
 SOURCE: Journal of Biochemistry (Tokyo) (1999), 125(4), 728-736

CODEN: JOBIAO; ISSN: 0021-924X

PUBLISHER: Japanese Biochemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A novel fungal **.beta.-glucosidase** gene (*bgl4*) and its homolog (*bgl2*) were cloned from the cellulolytic fungi *Humicola grisea* and *Trichoderma reesei*, resp. The deduced amino acid sequences of *H. grisea* BGL4 and *T. reesei* BGL2 comprise 476 and 466 amino acids, resp., and share 73.1% identity. These **.beta.-glucosidases** show significant homol. to plant **.beta.-glucosidases** belonging to the **.beta.-glucosidase** A (BGA) family. Both genes were expressed in *Aspergillus oryzae*, and the recombinant **.beta.-glucosidases** were purified. Recombinant *H. grisea* BGL4 is a thermostable enzyme compared with recombinant *T. reesei* BGL2. In addn. to **.beta.-glucosidase** activity, recombinant *H. grisea* BGL4 showed a significant level of **.beta.-galactosidase** activity, while recombinant *T. reesei* BGL2 showed weak **.beta.-galactosidase** activity. Cellulose saccharification by *Trichoderma* cellulases was improved by the addn. of recombinant *H. grisea* BGL4.

REFERENCE COUNT: 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 2

ACCESSION NUMBER: 1998:486295 CAPLUS

DOCUMENT NUMBER: 129:198717

TITLE: Identification, sequence analysis and expression studies of novel anther-specific genes of *Arabidopsis thaliana*

AUTHOR(S): Rubinelli, Peter; Hu, Yi; Ma, Hong

CORPORATE SOURCE: Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 11724, USA

SOURCE: Plant Molecular Biology (1998), 37(4), 607-619

CODEN: PMBIDB; ISSN: 0167-4412

PUBLISHER: Kluwer Academic Publishers

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Relatively little is known about pollen development at the mol. level. For the purpose of gaining understanding of the mol. control of pollen development, a no. of *Arabidopsis* cDNA fragments were isolated using subtractive hybridizations. DNA and RNA hybridizations and sequence analyses indicate that the authors have isolated cDNAs representing 13 genes. Sequences for 8 of these genes are novel, while those for the remaining 5 genes have substantial similarity to genes previously reported as anther- or pollen-specific. RNA in situ hybridizations with 5 genes revealed that four of them are tapetum-specific with differing temporal expression patterns during pollen development and one is pollen-specific within the flower. Sequence anal. of full-length cDNAs showed that one of the novel genes, ATA7, encodes a protein related to lipid transfer proteins. Another gene, ATA20, encodes a protein with novel repeat sequences and a glycine-rich domain that shares a predicted structure with a known cell wall protein. The full-length ATA27 cDNA encodes a protein similar to the BGL4 **.beta.-glucosidase** from *Brassica napus*. The ATA27 protein is predicted to have an ER retention signal and an acidic isoelec. point, suggesting that it may be localized to the ER lumen. This may be a means of compartmentalization from its substrate(s). These studies demonstrate that subtractive hybridizations can be used to identify previously unknown genes, which should be valuable tools for further study of pollen and anther development and function.

REFERENCE COUNT: 48 THERE ARE 48 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2003 ACS

DUPLICATE 1

ACCESSION NUMBER: 1999:348867 CAPLUS

DOCUMENT NUMBER: 131:155115

TITLE: Molecular cloning and expression of the novel fungal .
beta.-glucosidase genes from
Humicola grisea and **Trichoderma**
reesei

AUTHOR(S): Takashima, Shou; Nakamura, Akira; Hidaka, Makoto;
Masaki, Haruhiko; Uozumi, Takeshi

CORPORATE SOURCE: Department of Biotechnology, Graduate School of
Agricultural and Life Sciences, The University of
Tokyo, Tokyo, 113-8657, Japan

SOURCE: Journal of Biochemistry (Tokyo) (1999), 125(4),
728-736

CODEN: JOBIAO; ISSN: 0021-924X

PUBLISHER: Japanese Biochemical Society

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A novel fungal **.beta.-glucosidase** gene (**bgl4**
) and its homolog (**bgl2**) were cloned from the cellulolytic fungi *Humicola*
grisea and **Trichoderma reesei**, resp. The deduced
amino acid sequences of *H. grisea* **BGL4** and *T. reesei*
BGL2 comprise 476 and 466 amino acids, resp., and share 73.1% identity.
These **.beta.-glucosidases** show significant homol. to
plant **.beta.-glucosidases** belonging to the .
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is a thermostable enzyme compared with recombinant *T. reesei*
BGL2. In addn. to **.beta.-glucosidase** activity,
recombinant *H. grisea* **BGL4** showed a significant level of
.beta.-galactosidase activity, while recombinant *T. reesei* **BGL2**
showed weak **.beta.-galactosidase** activity. Cellulose saccharification by
Trichoderma cellulases was improved by the addn. of recombinant *H.*
grisea **BGL4**.

REFERENCE COUNT: 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS
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END OF SEARCH HISTORY